

GenCore version 5.1.6
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OH nucleic - nucleic search, using sw model
Run on: August 6, 2003, 13:01:34 ; Search time 2 Seconds
(without alignments)
2.904 Million cell updates/sec

Title: us-10-036-041-1
Perfect score: 1712
Sequence: 1 ggcatctgcggaggagacc.....ttgttaaagaaaaaaa 1712

Scoring table: IDENTITY_NDC
Gapop 10.0 , Gapext 0.5
Searched: 1 seqs, 1636 residues

Total number of hits satisfying chosen parameters: 2
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 10%
Listing first 1 summaries

Database : us-09-552-225a-1:
us-09-552-225a-1:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description	
1	1696	99.1	1696	1 us-09-552-225a-1	

ALIGNMENTS					
RESULT 1 us-09-552-225a-1					
Query Match Best Local Similarity	99.1% ; Score 1696; DB 1;	Length 1696;			
Matches 1696; Conservative	100.0% ; Pfd. No. 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY 9	CCGGAGGAGACCACGCMTCCTGGAGCTCNGCTGCGTCAAGGGAGACTCTGAGGCTCTGT	68	Db 1	CCGGAGGAGACCACGCMTCCTGGAGCTCAGCTCAAGGGAGACTCTGAGGCTCTGT	60
QY 129	CTTTTGCGCTGTCAAGTGATACTGAGAATCATGGAGCTCTCCACAAACCGGAGACTACCCCCAG	188	Db 121	CTTTTGCCTGTCAAGTGATACTGAGAATCATGGAGCTCTCCACAAACCGGAGACTACCCCCAG	180
QY 189	ACTGCASTPAAGCTGTCATGGAGACPAAGCTTTCGAGGCTACCAAGGCCCTGGGC	248	Db 181	ACTGCASTPAAGCTGTCATGGAGACPAAGCTTTCGAGGCTACCAAGGCCCTGGGC	240
QY 249	CACGGGCCCTCTGGCATTCAGGAACATGGCAACATGGAGGCCACTG	308	Db 241	CACGGGCCCTCTGGCATTCAGGAACATGGCAACATGGAGGCCACTG	300
QY 1389	ATAGATTAGCTTACGTTAACGTGCTTGTAAATGTGGTTGCAATGTC	1448	QY		
309	GTCACTGAGGGCCAAAGTGAGAAGGGGACAAAGGCTGACCCMGGGCTCGAGGGAGC	368	QY		
301	GTCACTGAGGGCCAAAGTGAGAAGGGCAGACAAAGGTGACCTGGCCCTCGAGGGAGC	360	Db		
369	GGGGCAGCATGGCCAAGGGAGAAGGGTACCCGGGAPTCACCCAGAACTCTAGA	428	QY		
361	GGGGCAGCATGGCCAAGGGGATCACCGGGATCAGCAACTCAGCAACTCAGA	420	Db		
429	TTGCAATCATGGCTCTGGCAACCACTTCAGCAACTCAGCAACTCAGCAACTCAGA	488	QY		
421	TTGCAATCATGGCTCTGGCAACCACTTCAGCAACTCAGCAACTCAGCAACTCAGA	480	Db		
489	GCAGTGTTGAGACCAACATGGAAACATCTGAGCTATGACTGAGATTTGGGGCC	548	QY		
481	GCAGTGTTGAGACCAACATGGAAACATCTGAGCTATGACTGAGATTTGGGGCC	540	Db		
549	CACTATCAGGTGTTGATTCCTCACCTCACCTCACCTCACCTCACCTCACCTCAC	608	QY		
541	CACTATCAGGTGTTGATTCCTCACCTCACCTCACCTCACCTCACCTCACCTCAC	600	Db		
609	TGATGTTACCTTACGATGGCAACACTCTGAGCTAGCTAGTAAGAATGA	668	QY		
601	TGATGTTACCTTACGATGGCAACACTCTGAGCTAGCTAGTAAGTATGATG	660	Db		
669	AGGCCAAATCAGATACTCCAGAAATCATGCTGCTGAGCTAGCCAAAGGGATGAGG	728	QY		
661	AGGCCAAATCAGATACTCCAGAAATCATGCTGCTGAGCTAGCCAAAGGGATGAGG	720	Db		
729	TTGGCTGGAAATGGCAATGGCTCCTTCATGGCAATGGCAATGGCAATGGCA	788	QY		
721	TTGGCTGGAAATGGCAATGGCTCCTTCATGGCAATGGCAATGGCAATGGCA	780	Db		
789	CAGGATTCCTGCCTTCGAACACTAATGAGTAAATATGACTAGATACTGGCA	848	QY		
781	CAGGATTCCTGCCTTCGAACACTAATGAGTAAATATGACTAGATACTGGCA	840	Db		
849	AGACTGTAGCTGAGCTGATCTGAGCTGAGCAATTAAGTGGGTTTACA	908	QY		
841	AGACTGTAGCTGAGCTGATCTGAGCTGATCTGAGCTGAGCTGAGCTG	900	Db		
909	TTGCTGTATTCAAAATTATTGGTCAATTTGTTCACTGTTGAGCTACAGCTAC	968	QY		
901	TTGCTGTATTCAAAATTATTGGTCAATTTGTTCACTGTTGAGCTACAGCTAC	960	Db		
969	GTGGACATTCTGGCTCAGAGATCAACCAAAATAGTCTGAGCTGCTG	1028	QY		
961	GTGGACATTCTGGCTCAGAGATCAACCAAAATAGTCTGAGCTGCTG	1020	Db		
1029	ACTAATAFACTCAGCATTTAACATCTTTCCTGACCTAAAGATAATTCTCC	1088	QY		
1021	ACTAATAFACTCAGCATTTAACATCTCCTTCCTGACCTAAAGATAATTCTCC	1080	Db		
1089	GACGCCAGTTGGAAATATTTCATCACAGAACTCATTCAGAACTATTGCTAC	1148	QY		
1081	GACCCAGTTGGCAACCTTCAGTTGAGCTACATTTTCATCACAGAACTATTGCTAC	1140	Db		
1149	TCTGGCTTTTAAATTATPACGAGTTTCTGAGACCCCTGAGTTTAACTCTATTC	1208	QY		
1141	TCTGGCTTTTAAATTATPACGAGTTTCTGAGACCCCTGAGTTTAACTCTATTC	1200	Db		
1209	TATAACATTGAGAATCGGATGTAATGATACTGAGCTACATTTTCATCACAGAA	1268	QY		
1201	TATAACATTGAGAATCGGATGTAATGATACTGAGCTACATTTTCATCACAGAA	1260	Db		
1269	CTAGCTGCCTTATTAGCTTAATTAGCTTAATTAGCTTCGCTTCTGAGCTTC	1328	QY		
1261	CTAGCTGCCTTATTAGCTTAATTAGCTTCGCTTCTGAGCTTC	1320	Db		
1329	CTTGTGTCACAAATACATGATCTGATCTGATCTGATCTGATCTGATCTG	1388	QY		
1321	CTTGTGTCACAAATACATGATCTGATCTGATCTGATCTGATCTGATCTG	1380	Db		

Db	1381	AATGATTCTAGCTATAAAGTGCYTGACCAAGTATGTGGTTGTAATTGTGTATGTC	CC 1440
Qy	1449	CCCATCCCCCACAATCGGATGGGTCAAGGTTGAGTTCACTATTAAACATG	1508
Db	1441	CCACATCCCCACAATCGGATGGGTCAAGGTTGAGTTCACTATTAAACATG	1500
Qy	1509	TCTAAATAATCTCATAGGGTACAGTGCCAAATAGATATTCAAATGTTGACAG	1568
Db	1501	TCTAAATAATCTCATAGGGTACAGTGCCAAATAGATATTCAAATGTTGACAG	1560
Qy	1569	AGGGATTTTATATCTGAGAACATAACATTAAATACCTTAGAGAAAGATTGAC	1628
Db	1561	AGGGATTTTATATCTGAGAACATAACATTAAATACCTTAGAGAAAGATTGAC	1620
Qy	1629	CAGGCTTTAGATAAACCTGGCAAGAAAATGTAATGAGCAATAATGAAAC	1688
Db	1621	CAGGCTTTAGATAAACCTGGCAAGAAAATGTAATGAGCAATAATGAAAC	1680
Qy	1669	ACCTTTGTTAAAGATA	1704
Db	1681	ACCTTTGTTAAAGATA	1696

Search completed: August 6, 2003, 13:01:36
 Job time : 2 secs

